

SYN-128.ST25.txt
SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic
Combinations Thereof

<130> SYN-128

<140> US 10/019,823

<141> 2001-12-21

<150> PCT/GB00/02457

<151> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 33

<212> PRT

<213> Paecilomyces sp.

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 1

Xaa	Xaa	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
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Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 2

<211> 33

<212> PRT

<213> Paecilomyces sp.

<400> 2

Gly	Lys	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
1				5				10						15	
Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 3

<211> 35

<212> PRT

<213> Paecilomyces sp.

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<220>

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<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 3

Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
 1 5 10 15
 Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
 20 25 30
 Val Cys Arg
 35

<210> 4

<211> 332

<212> DNA

<213> Paecilomyces sp.

<400> 4

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 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180
 ataacaatgac gcagtatact aaccctggcc gttatagaac aaggttgtga gtcgacatgt 240
 tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300
 gcaacttttg agcgtgggat aagtatgctt cg 332

<210> 5

<211> 320

<212> DNA

<213> Paecilomyces sp.

<400> 5

gggaaaattt gtacgccggc ggggggttgta cgtatttctca tccatttcct ccaccactcc 60
 tctaacaatga agcaactctc tcttctctct agaaatgtcc cgcggtctct ccttgctgcc 120
 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
 aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
 acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
 cgtgggataa gtatgcttcg 320

<210> 6

<211> 320

<212> DNA

<213> Paecilomyces sp.

<400> 6

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 tctaacaatga agcaactctc tcttctctct araaatgtcc cgcggtctct ccttgctgcc 120
 ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
 aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
 acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
 cgtgggataa gtatgcttcg 320

<210> 7

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 7

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60

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gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctccc 120
tgctgcccgg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga 174

<210> 8

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic polynucleotide codon optimised

<400> 8

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gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctccc 120
tgttgtccgg gcctcagggtg tattggtggt gtgaataata aagtgtgtcg ctga 174

<210> 9

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron sequence

<400> 9

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gagatccagg ccggcaagat ctgcactcct gctggagttg ttgttttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tataatgacca aaacatgggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgcccccg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363

<210> 10

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 10

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gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaatat 180
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240
tatattttaa tttataactt ttctaataata tgacaaaac atgggtgatgt ttagaaatgt 300
cccgcggctc ttccttgctg ccccggaact cgctgcatcg gcggcgtcaa caacaagggt 360
tgccggtaa 369

<210> 11

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 11

atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacat ctgcactcct gctggagttg ttgttttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240

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ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363

<210> 12
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing intron and codon
optimised

<400> 12
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gagatccagg ccggcaagat ctgcaccccg gccggcgtgg ttgtttctg cttctacctt 120
tgatataatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa gtgcccggcc 300
gccctcccggt gctgccccgg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga 363

<210> 13
<211> 439
<212> DNA
<213> Paecilomyces sp.

<400> 13
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aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcatcc atttccctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgc ggctcttctt tgctgccccg gacttcgctg 240
catcgccggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420
gtgggataag tatgcttcg 439

<210> 14
<211> 102
<212> DNA
<213> Paecilomyces sp.

<400> 14
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cttcgctgca tcggcggcgt caacaacaag gtttgccggt aa 102

<210> 15
<211> 84
<212> DNA
<213> Dahlia sp.

<400> 15
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tcagatatgg cttctgtttc agga 84

<210> 16
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Radish signal sequence

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<400> 16
atggctaagt ttgcttctat tattgctctt ttgtttgctg cacttgtttt gtttgctgca 60
tttgaagctc caactatggt tgaagct 87

<210> 17
<211> 72
<212> DNA
<213> Zea mays

<400> 17
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cc 72

<210> 18
<211> 90
<212> DNA
<213> Nicotiana sp.

<400> 18
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ttcctagtaa tatccactc ttgccgtgcc 90

<210> 19
<211> 51
<212> DNA
<213> Paecilomyces sp.

<400> 19
atgcaaactc cgcgcgtcat tgctgcactc ttcgccagcg ccgccatggc c 51

<210> 20
<211> 28
<212> PRT
<213> Dahlia sp.

<400> 20
Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
1 5 10 15
Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
20 25

<210> 21
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Radish protein target sequence

<400> 21
Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
1 5 10 15
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
20 25

<210> 22
<211> 24
<212> PRT
<213> Zea Mays

<400> 22

SYN-128.ST25.txt

Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
 1 5 10 15
 Ser Leu Ala Val Glu Ile Gln Ala
 20

<210> 23
 <211> 30
 <212> PRT
 <213> Nicotiana sp.

<400> 23
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1 5 10 15
 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
 20 25 30

<210> 24
 <211> 17
 <212> PRT
 <213> Paecilomyces sp.

<400> 24
 Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
 1 5 10 15
 Ala

<210> 25
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

<400> 25
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<210> 26
 <211> 19
 <212> DNA
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<220>
 <223> Primers

<400> 26
 tcgggctcgc atgaattcg 19

<210> 27
 <211> 18
 <212> DNA
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 <223> Primers

<400> 27
 atgaattcgc ggccgcat 18

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 28
 tcgggctcgc atgaattcgc g 21

 <210> 29
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 <400> 29
 ctcgcatgaa ttcgcggccg c 21

 <210> 30
 <211> 17
 <212> DNA
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 <220>
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 <221> misc_feature
 <222> 9, 12, 15
 <223> n = A,T,C or G

 <400> 30
 athtgyacnc cngcngg 17

 <210> 31
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 <220>
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 <221> misc_feature
 <222> 9, 12, 15, 18
 <223> n = A,T,C or G

 <400> 31
 athtgyacnc cngcnggngt 20

 <210> 32
 <211> 17
 <212> DNA
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 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 9, 12, 15
 <223> n = A,T,C or G

<400> 32 acnccngcng gngtnaa	17
<210> 33 <211> 17 <212> DNA <213> Artificial Sequence	
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<221> misc_feature <222> 3, 6, 18 <223> n = A,T,C or G	
<400> 35 ggngtnaaya ayaargtntg	20
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<210> 37
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<221> misc_feature
 <222> 3, 6, 9, 12, 21, 24
 <223> n = inosine

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 ccngcnggng tnaartgycc ngcngc

26

<210> 38
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 <223> Primers

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26

<210> 39
 <211> 26
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<220>
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 <222> 9, 12, 15
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26

<210> 40
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 40
 taaatgtccc gcggctcttc c

21

<210> 41
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<220>

<223> Primers
 <400> 41
 cggtctttcc ttgctgcccc g 21
 <210> 42
 <211> 21
 <212> DNA
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 <223> Primers
 <400> 42
 tgctgccccg gacttcgctg c 21
 <210> 43
 <211> 27
 <212> DNA
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 <220>
 <223> Primers
 <221> misc_feature
 <222> 23, 24, 25, 26, 27
 <223> n = A,T,C or G
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 <210> 44
 <211> 22
 <212> DNA
 <213> Artificial Sequence
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 <223> Primers
 <400> 44
 ctcaaacttg ggtaattaaa cc 22
 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <400> 45
 ggtttaatta cccaagtt 18
 <210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence
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 <223> Primers
 <400> 46
 taattacca agtttgag 18

<210> 47
 <211> 22
 <212> DNA
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 <400> 47
 ggtttaatta cccaagtttg ag 22

 <210> 48
 <211> 23
 <212> DNA
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 <223> Primers

 <221> misc_feature
 <222> 3, 15, 18, 21
 <223> n = inosine

 <400> 48
 canacyttrt trttnacncc ncc 23

 <210> 49
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 <400> 49
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 <210> 50
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 <400> 50
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 <210> 51
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 <400> 51
 aagagccgcg ggacatttaa c 21

 <210> 52
 <211> 49
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 52

agttaaatgt cccgcggctc ttccttgctg ccccggaactt cgctgcatc

49

<210> 53

<211> 18

<212> DNA

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<223> Primers

<400> 53

gatgcagcga agtccggg

18

<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

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<223> PROTEIN cryIIa1 Embl. Accession No. X62821

<221> VARIANT

<222> 602

<223> Xaa = Any Amino Acid

<400> 54

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      20      25      30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
      35      40      45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
      50      55      60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65      70      75      80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
      85      90      95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
      100      105      110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
      115      120      125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
      130      135      140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145      150      155      160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
      165      170      175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
      180      185      190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
      195      200      205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
      210      215      220
Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
225      230      235      240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg

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SIN-128.3125.txt															
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Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305	Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu
310	Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp
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330	Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn
335	Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr
350	Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val
355	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile
360	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln
365	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro
370	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
375	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
385	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
390	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
400	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Thr	Asn	Thr	Thr	Gly	Thr	Phe
405	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
410	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
415	Asn	Gly	Lys	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn	Arg
420	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Xaa	Thr	Val	Gly	Phe	Thr	Thr
425	Pro	Phe	Ser	Leu	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
430	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
435	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
440	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
445	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
450	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Gln	Leu	Lys	Arg	Glu	Leu	Phe	Glu
455	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met			
460	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
465	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
470	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
475	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
480	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
485	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
490	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
495	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
500	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
505	Val	Lys	Tyr	Ala	Lys	Gln	Ile	Glu	Arg	Asn	Met				
510	Val	Lys	Tyr	Ala	Lys	Gln	Ile								

<210>	55
<211>	719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cryIIa2 Emb1. Accession No. M98544

<400> 55

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1      5      10      15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20      25      30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35      40      45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50      55      60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65      70      75      80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85      90      95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100      105      110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115      120      125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130      135      140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145      150      155      160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165      170      175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
180      185      190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
195      200      205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
210      215      220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225      230      235      240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
245      250      255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
260      265      270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
275      280      285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
290      295      300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305      310      315      320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
325      330      335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
340      345      350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355      360      365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370      375      380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385      390      395      400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405      410      415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
420      425      430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
435      440      445

```

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Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
450 455 460
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
465 470 475
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
485 490 495
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
500 505 510
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
515 520 525
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
530 535 540
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
545 550 555
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
565 570 575
Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
580 585 590
Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
595 600 605
Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
610 615 620
Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
625 630 635
Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
645 650 655
Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
660 665 670
Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
675 680 685
Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
690 695 700
Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
705 710 715

```

<210> 56
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN cry1Ia3 Emb1. Accession No. L36338

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<400> 56
Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
1 5 10 15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
20 25 30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
35 40 45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
50 55 60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65 70 75 80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
85 90 95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100 105 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115 120 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130 135 140

```

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Trp 145	Val	Gly	Asn	Arg	Asn 150	Asn	Thr	Arg	Ala	Arg 155	Ser	Val	Val	Lys	Ser 160
Gln	Tyr	Ile	Ala	Leu 165	Glu	Leu	Met	Phe	Val 170	Gln	Lys	Leu	Pro	Ser 175	Phe
Ala	Val	Ser	Gly 180	Glu	Glu	Val	Pro	Leu 185	Leu	Pro	Ile	Tyr	Ala 190	Gln	Ala
Ala	Asn	Leu 195	His	Leu	Leu	Leu	Leu 200	Arg	Asp	Ala	Ser	Ile 205	Phe	Gly	Lys
Glu	Trp 210	Gly	Leu	Ser	Ser	Ser 215	Glu	Ile	Ser	Thr	Phe 220	Tyr	Asn	Arg	Gln
Val 225	Glu	Arg	Ala	Gly	Asp 230	Tyr	Ser	Tyr	His	Cys 235	Val	Lys	Trp	Tyr	Ser 240
Thr	Gly	Leu	Asn	Asn 245	Leu	Arg	Gly	Thr	Asn 250	Ala	Glu	Ser	Trp	Val 255	Arg
Tyr	Asn	Gln	Phe 260	Arg	Arg	Asp	Met	Thr 265	Leu	Met	Val	Leu	Asp 270	Leu	Val
Ala	Leu	Phe 275	Pro	Ser	Tyr	Asp	Thr 280	Gln	Met	Tyr	Pro	Ile 285	Lys	Thr	Thr
Ala	Gln 290	Leu	Thr	Arg	Glu	Val 295	Tyr	Thr	Asp	Ala	Ile 300	Gly	Thr	Val	His
Pro 305	His	Pro	Ser	Phe	Thr 310	Ser	Thr	Thr	Trp	Tyr 315	Asn	Asn	Asn	Ala	Pro 320
Ser	Phe	Ser	Ala	Ile 325	Glu	Ala	Ala	Val	Val 330	Arg	Asn	Pro	His	Leu 335	Leu
Asp	Phe	Leu	Glu 340	Gln	Val	Thr	Ile	Tyr 345	Ser	Leu	Leu	Ser	Arg 350	Trp	Ser
Asn	Thr	Gln 355	Tyr	Met	Asn	Met	Trp 360	Gly	Gly	His	Lys	Leu 365	Glu	Phe	Arg
Thr	Ile 370	Gly	Gly	Thr	Leu	Asn 375	Ile	Ser	Thr	Gln	Gly 380	Ser	Thr	Asn	Thr
Ser 385	Ile	Asn	Pro	Val	Thr 390	Leu	Pro	Phe	Thr	Ser 395	Arg	Asp	Val	Tyr	Arg 400
Thr	Glu	Ser	Leu	Ala 405	Gly	Leu	Asn	Leu	Phe 410	Leu	Thr	Gln	Pro	Val 415	Asn
Gly	Val	Pro	Arg 420	Val	Asp	Phe	His	Trp 425	Lys	Phe	Val	Thr	His 430	Pro	Ile
Ala	Ser	Asp 435	Asn	Phe	Tyr	Tyr	Pro 440	Gly	Tyr	Ala	Gly	Ile 445	Gly	Thr	Gln
Leu	Gln 450	Asp	Ser	Glu	Asn	Glu 455	Leu	Pro	Pro	Glu	Ala 460	Thr	Gly	Gln	Pro
Asn 465	Tyr	Glu	Ser	Tyr	Ser 470	His	Arg	Leu	Ser	His 475	Ile	Gly	Leu	Ile	Ser 480
Ala	Ser	His	Val	Lys 485	Ala	Leu	Val	Tyr	Ser 490	Trp	Thr	His	Arg	Ser 495	Ala
Asp	Arg	Thr	Asn 500	Thr	Ile	Glu	Pro	Asn 505	Ser	Ile	Thr	Gln	Ile 510	Pro	Leu
Val	Lys	Ala 515	Phe	Asn	Leu	Ser	Ser 520	Gly	Ala	Ala	Val	Val 525	Arg	Gly	Pro
Gly	Phe 530	Thr	Gly	Gly	Asp	Ile 535	Leu	Arg	Arg	Thr	Asn 540	Thr	Gly	Thr	Phe
Gly 545	Asp	Ile	Arg	Val	Asn 550	Ile	Asn	Pro	Pro	Phe 555	Ala	Gln	Arg	Tyr	Arg 560
Val	Arg	Ile	Arg	Tyr 565	Ala	Ser	Thr	Thr	Asp 570	Leu	Gln	Phe	His	Thr 575	Ser
Ile	Asn	Gly	Lys 580	Ala	Ile	Asn	Gln	Gly 585	Asn	Phe	Ser	Ala	Thr 590	Met	Asn
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys 600	Thr	Phe	Arg	Thr	Val 605	Gly	Phe	Thr
Thr	Pro 610	Phe	Ser	Phe	Leu	Asp 615	Val	Gln	Ser	Thr	Phe 620	Thr	Ile	Gly	Ala
Trp 625	Asn	Phe	Ser	Ser	Gly 630	Asn	Glu	Val	Tyr	Ile 635	Asp	Arg	Ile	Glu	Phe 640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala

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Gln	Glu	Lys	Val	645	Thr	Ala	Leu	Phe	Thr	650	Ser	Thr	Asn	Pro	Arg	655	Gly	Leu
Lys	Thr	Asp	660	Val	Lys	Asp	Tyr	His	665	Ile	Asp	Gln	Val	Ser	670	Asn	Leu	Val
Glu	Ser	Leu	675	Ser	Asp	Glu	Phe	Tyr	680	Leu	Asp	Glu	Lys	Arg	685	Glu	Leu	Phe
Glu	Ile	Val	690	Lys	Tyr	Ala	Asn	Glu	695	Leu	His	Ile	700	Glu	Arg	Asn	Met	
705						710						715						

<210> 57
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN cry1Ia4 Emb1. Accession No. L49391

<400> 57

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala			
1				5					10					15				
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile			
			20					25					30					
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr			
		35					40					45						
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile			
	50					55					60							
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly			
65					70				75						80			
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys			
			85						90					95				
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile			
		100						105					110					
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu			
		115					120					125						
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser			
	130					135					140							
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser			
145					150				155					160				
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe			
			165					170						175				
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala			
		180					185						190					
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys			
		195				200						205						
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln			
	210					215					220							
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Ser			
225					230					235					240			
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg			
			245						250					255				
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val			
		260						265					270					
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr			
		275					280					285						
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His			
	290					295					300							
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro			
305					310					315					320			
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu			
			325					330						335				
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser			

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340
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
400
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
415
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Val Gly Ile Gly Thr Gln
430
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
445
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
460
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
475
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
490
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
505
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
520
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
535
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
550
Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
565
Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
580
Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
595
Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
610
Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
625
Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
630
Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
645
Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
660
Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
675
705
710
715

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<210> 58

<211> 719

<212> PRT

<213> Artificial sequence

<220>

<223> PROTEIN cry1Ia5 Embl. Accession No. Y08920

<400> 58

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
1      5      10
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
20     25     30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr

```



		35					40					45			
Glu 60	Asn 50	Val	Glu	Pro	Phe	Val 55	Ser	Ala	Ser	Thr	Ile 60	Gln	Thr	Gly	Ile
Gly 65	Ile	Ala	Gly	Lys	Ile 70	Leu	Gly	Thr	Leu	Gly 75	Val	Pro	Phe	Ala	Gly 80
Gln	Val	Ala	Ser	Leu 85	Tyr	Ser	Phe	Ile	Leu 90	Gly	Glu	Leu	Trp	Pro 95	Lys
Gly	Lys	Asn 100	Gln	Trp	Glu	Ile	Leu	Phe 105	Met	Glu	His	Val	Glu 110	Glu	Ile
Asn	Gln	Lys 115	Ile	Ser	Thr	Tyr	Ala 120	Arg	Asn	Lys	Ala	Leu 125	Thr	Asp	Leu
Lys	Gly 130	Leu	Gly	Asp	Ala	Leu 135	Ala	Val	Tyr	His	Asp 140	Ser	Leu	Glu	Ser
Trp 145	Val	Gly	Asn	Arg	Asn 150	Asn	Thr	Arg	Ala	Arg 155	Ser	Val	Val	Arg	Ser 160
Gln	Tyr	Ile	Ala	Leu 165	Glu	Leu	Met	Phe	Val 170	Gln	Lys	Leu	Pro	Ser 175	Phe
Ala	Val	Ser	Gly 180	Glu	Glu	Val	Pro	Leu 185	Leu	Pro	Ile	Tyr	Ala 190	Gln	Ala
Ala	Asn	Leu 195	His	Leu	Leu	Leu	Leu 200	Arg	Asp	Ala	Ser	Ile 205	Phe	Gly	Lys
Glu	Trp 210	Gly	Leu	Ser	Ser	Ser 215	Glu	Ile	Ser	Thr	Phe 220	Tyr	Asn	Arg	Gln
Val	Glu	Arg	Ala	Gly	Asp 230	Tyr	Ser	Asp	His	Cys 235	Val	Lys	Trp	Tyr	Ser 240
Thr	Gly	Leu	Asn	Asn 245	Leu	Arg	Gly	Thr	Asn 250	Ala	Glu	Ser	Trp	Val 255	Arg
Tyr	Asn	Gln	Phe 260	Arg	Arg	Asp	Met	Thr 265	Leu	Met	Val	Leu	Asp 270	Leu	Val
Ala	Leu	Phe 275	Pro	Ser	Tyr	Asp	Thr 280	Gln	Met	Tyr	Pro	Ile 285	Lys	Thr	Thr
Ala	Gln 290	Leu	Thr	Arg	Glu	Val 295	Tyr	Thr	Asp	Ala	Ile 300	Gly	Thr	Val	His
Pro 305	His	Pro	Ser	Phe	Thr 310	Ser	Thr	Thr	Trp	Tyr 315	Asn	Asn	Asn	Ala	Pro 320
Ser	Phe	Ser	Ala	Ile 325	Glu	Ala	Ala	Val	Val 330	Arg	Asn	Pro	His	Leu 335	Leu
Asp	Phe	Leu	Glu 340	Gln	Val	Thr	Ile	Tyr 345	Ser	Leu	Leu	Ser	Arg 350	Trp	Ser
Asn	Thr	Gln 355	Tyr	Met	Asn	Met	Trp 360	Gly	Gly	His	Lys	Leu 365	Glu	Phe	Arg
Thr	Ile 370	Gly	Gly	Thr	Leu	Asn 375	Ile	Ser	Thr	Gln	Gly 380	Ser	Thr	Asn	Thr
Ser 385	Ile	Asn	Pro	Val	Thr 390	Leu	Pro	Phe	Thr	Ser 395	Arg	Asp	Val	Tyr	Arg 400
Thr	Glu	Ser	Leu	Ala 405	Gly	Leu	Asn	Leu	Phe 410	Leu	Thr	Gln	Pro	Val 415	Asn
Gly	Val	Pro	Arg 420	Val	Asp	Phe	His	Trp 425	Lys	Phe	Val	Thr	His	Pro	Ile
Ala	Ser	Asp 435	Asn	Phe	Tyr	Tyr	Pro 440	Gly	Tyr	Ala	Gly	Ile 445	Gly	Thr	Gln
Leu	Gln	Asp	Ser	Glu	Asn	Glu 455	Leu	Pro	Pro	Glu	Ala 460	Thr	Gly	Gln	Pro
Asn 465	Tyr	Glu	Ser	Tyr	Ser 470	His	Arg	Leu	Ser	His 475	Ile	Gly	Leu	Ile	Ser 480
Ala	Ser	His	Val	Lys 485	Ala	Leu	Val	Tyr	Ser 490	Trp	Thr	His	Arg	Ser 495	Ala
Asp	Arg	Thr	Asn 500	Thr	Ile	Glu	Pro	Asn 505	Ser	Ile	Thr	Gln	Ile 510	Pro	Leu
Val	Lys	Ala 515	Phe	Asn	Leu	Ser	Ser 520	Gly	Ala	Ala	Val	Val 525	Arg	Gly	Pro
Gly	Phe 530	Thr	Gly	Gly	Asp	Ile 535	Leu	Arg	Arg	Thr	Asn 540	Thr	Gly	Thr	Phe

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Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Asn	Glu	Leu	His	Ile	Glu	Arg	Asn	Met	
705					710					715					

<210> 59

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ib1 Emb1. Accession No. U07642

<400> 59

Met	Lys	Leu	Lys	Asn	Pro	Asp	Lys	His	Gln	Ser	Leu	Ser	Ser	Asn	Ala
1				5					10					15	
Lys	Val	Asp	Lys	Ile	Ala	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile
			20					25					30		
Glu	Leu	Lys	Asn	Met	Asn	Asn	Glu	Asp	Tyr	Leu	Arg	Met	Ser	Glu	His
		35					40					45			
Glu	Ser	Ile	Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55				60					
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65					70				75						80
Gln	Ile	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
			85						90					95	
Gly	Lys	Ser	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100					105					110		
Asn	Gln	Lys	Ile	Leu	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Asp	Leu
		115					120					125			
Arg	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Glu	Ser	Leu	Glu	Ser
	130					135					140				
Trp	Val	Glu	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Asn
145					150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
			165						170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
			180					185					190		
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
		195					200					205			
Glu	Trp	Gly	Leu	Ser	Ala	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Thr	Arg	Asp	Tyr	Ser	Asp	His	Cys	Ile	Lys	Trp	Tyr	Asn
225					230					235					240

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Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Lys	Ser	Trp	Val	Arg
				245					250					255	
Tyr	Asn	Gln	Phe	Arg	Lys	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
			260					265					270		
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Leu	Val	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ser	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295					300				
Pro	Asn	Gln	Ala	Phe	Ala	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Ile	Arg	Ser	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Lys	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
			340					345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Arg	Leu	Glu	Ser	Arg
		355					360					365			
Pro	Ile	Gly	Gly	Ala	Leu	Asn	Thr	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Gln	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
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Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Pro	Thr	Leu	Pro	Ile
			420					425					430		
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Leu	Gly	Tyr	Ala	Gly	Val	Gly	Thr	Gln
		435					440					445			
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Thr	Thr	Gly	Gln	Pro
	450					455					460				
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465					470					475					480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
				485					490					495	
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
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Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
		515					520					525			
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
	530					535					540				
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Ile	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Ser	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
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ctcctgctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgc ggctcttctt tgctgccccg gacttcgctg 240
catcgccggc gtcaacgtaa gtcacccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
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cgccgctcatt gtcgcactct tcgccagcgc cgccatggcc ggcaagatct gcactcctgc 180
tggaagttaa tgtcccgcgg ctcttccttg ctgccccgga cttcgctgca tcggcggcgt 240
caacaacaag gtttgccggt aattctagtg tcgcaacttt tgagcgtggg ataagtatgc 300
ttcgttcgtt gtatggagtt ctctccgga gtttaagctc ggccggtcga cagcgggtct 360
gctatacttg atcttacagc gatactattg atagaaatgc acatcttcat tcatgctgca 420
tgaaaaaaaa aaaaaaaaa 438

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<213> Artificial Sequence

<220>
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<400> 63
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<210> 64
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
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 1 5

<210> 65
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 <220>
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 <221> VARIANT
 <222> 1, 2
 <223> Xaa = Any Amino Acid

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